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Assistant Commissioner for Patents
Washington, D.C. 20231

On May 23, 2002

TOWNSEND and TOWNSEND and CREW LLP

By: _____

PATENT
Attorney Docket No.: 021044-000600US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

MASUDA et al.

Application No.: 09/998,667

Filed: December 3, 2001

For: TRAC1: MODULATORS OF LYMPHOCYTE ACTIVATION

Examiner: Not yet assigned

Art Unit: 1653

INFORMATION DISCLOSURE STATEMENT UNDER 37 CFR §1.97 and §1.98

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

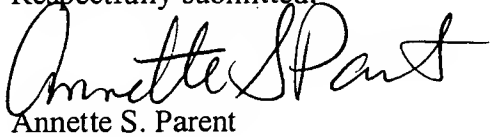
The references cited on attached form PTO/SB/08A and PTO/SB/08B are being called to the attention of the Examiner. Copies of the references are enclosed. It is respectfully requested that the cited references be expressly considered during the prosecution of this application, and the references be made of record therein and appear among the "references cited" on any patent to issue therefrom.

As provided for by 37 CFR 1.97(g) and (h), no inference should be made that the information and references cited are prior art merely because they are in this statement and no

representation is being made that a search has been conducted or that this statement encompasses all the possible relevant information.

Applicant believes that no fee is required for submission of this statement, since it is being submitted prior to the first Office Action. However, if a fee is required, the Commissioner is authorized to deduct such fee from the undersigned's Deposit Account No. 20-1430. Please deduct any additional fees from, or credit any overpayment to, the above-noted Deposit Account.

Respectfully submitted,



Annette S. Parent
Reg. No. 42,058

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San Francisco, California 94111-3834
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Fax: 415-576-0300
ASP:dk

SF 1349089 v1

PTO/SB/08A (10-01)
Approved for use through 10/31/2002. OMB 0651-0031
U.S. Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE
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Substitute for form 1449A/PTO

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(use as many sheets as necessary)

Sheet 1 of

Complete if Known	
Application Number	09/998,667
Filing Date	December 3, 2001
First Named Inventor	Masuda, Esteban
Art Unit	1653
Examiner Name	Not yet assigned
Attorney Docket Number	021044-000600US

U.S. PATENT DOCUMENTS

Examiner	Cite No.[1]	Document Number Number Kind Code[2] (*if known*)	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
	AA	US-			
	AB	US-			
	AC	US-			
	AD	US-			
	AE	US-			
	AF	US-			
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	AN	US-			
	AO	US-			
	AP	US-			
	AQ	US-			
	AR	US-			
	AS	US-			
	AT	US-			

FOREIGN PATENT DOCUMENTS

Examiner Initials*	Cite No.[1]	Foreign Patent Document Country Code[3] Number[4] Kind Code[5] (*if known*)	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T[6]
	AU					
	AV					
	AW					
	AX					
	AY					
	AZ					
	BA					
	BB					

Examiner Signature		Date Considered	

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

[1] Unique citation designation number. [2] See attached Kinds of U.S. Patent Documents. [3] Enter Office that issued the document, by the two-letter code (WIPO Standard ST.3). [4] For Japanese patent documents, the indication of the year of the reign of the Emperor must precede the serial number of the patent document. [5] Kind of document by the appropriate symbols as indicated on the document under WIPO Standard ST. 16 if possible. [6] Applicant is to place a check mark here if English language Translation is attached.

Burden Hour Statement: This form is estimated to take 2.0 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

PTO/SB/08B (10-01)
Approved for use through 10/31/2002. OMB 0651-0031
U.S. Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE
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Substitute for form 1449B/PTO

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(use as many sheets as necessary)

Sheet 2 of

Complete if Known	
Application Number	09/998,667
Filing Date	December 3, 2001
First Named Inventor	Masuda, Esteban
Art Unit	1653
Examiner Name	Not yet assigned
Attorney Docket Number	021044-000600US

OTHER PRIOR ART -- NON PATENT LITERATURE DOCUMENTS

Examiner Initials *	Cite No.[1]	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T[2]
	BC	Accession No. XM-008732, submitted 06 February 2002, National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	
	BD	Accession No. AK000463, submitted 15 February 2000, Sumio Sugano, Institute of Medical Science, University of Tokyo, Department of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan.	
	BE	Accession No. NM-017831, submitted 02/15/2000.	
	BF		
	BG		
	BH		
	BI		
	BJ		
	BK		
	BL		
	BM		

Examiner Signature		Date Considered	

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

[1] Unique citation designation number. [2] Applicant is to place a check mark here if English language Translation is attached.

Burden Hour Statement: This form is estimated to take 2.0 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

1: NM_017831. Homo sapiens hypo...[gi:8923428] Related Sequences, Protein, Taxonomy, LinkOut

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DEFINITION  Homo sapiens hypothetical protein FLJ20456 (FLJ20456), mRNA.
ACCESSION   NM_017831
VERSION     NM_017831.1  GI:8923428
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
            Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished (2000)
COMMENT     PREDICTED REFSEQ: The mRNA record is supported by experimental
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Revised: October 24, 2001.

Entrez Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM B

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1: AK000463. Homo sapiens cDNA...[gi:7020568] Related Sequences, Protein, Taxonomy, LinkOut

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ACCESSION   AK000463
VERSION     AK000463.1  GI:7020568
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SOURCE      Homo sapiens signet-ring cell carcinoma cell_line:KATO III cDNA to
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
            Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished (2000)
REFERENCE   2  (bases 1 to 1916)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1,
            Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna1@ims.u-tokyo.ac.jp,
            Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing: Departent of
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Revised: October 24, 2001.

1: XM_008732. Homo sapiens hypo...[gi:18588856] Related Sequences, Protein, Taxonomy, LinkOut

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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1916)
  AUTHORS   NCBI Annotation Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-2002) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
COMMENT     GENOME ANNOTATION REFSEQ:  This model reference sequence was
            predicted from NCBI contig NT_010966 by automated computational
            analysis using gene prediction method: BLAST. ~Also see:~
            Documentation of NCBI's Annotation Process~    Evidence Viewer -
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            On Feb 7, 2002 this sequence version replaced gi:17456245.
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  1861 acactccagc ctgggtaaca gagctagact ccatctcaaa aaaaaaaaaa aaaaaa
//
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Revised: October 24, 2001.

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On April 18, 2002

TOWNSEND and TOWNSEND and CREW LLP

By: Jane Love

PATENT
Attorney Docket No.: 021044-000600US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: MASUDA *et al.* Application No.: 09/998,667 Filed: December 3, 2001 For: TRAC1: MODULATORS OF LYMPHOCYTE ACTIVATION	Examiner: Not yet assigned Art Unit: 1653 COMMUNICATION UNDER 37 C.F.R. §§ 1.821-1.825 AND PRELIMINARY AMENDMENT

U.S. Patent and Trademark Office
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Arlington, VA 22202

Sir:

In response to the request to comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825, that accompanied the Notice to File Missing Parts of Nonprovisional Application mailed December 26, 2001, Applicants submit herewith the required paper copy and computer readable copy of the Sequence Listing. Please amend the specification in adherence with 37 C.F.R. §§ 1.821-1.825 as follows.

In the Specification:

Please replace the paragraph beginning at page 5, line 26, with the following:

--Figure 1: Figure 1A shows an amino acid of human wild-type TRAC1 (SEQ ID NO:1); Figure 1B shows a cDNA sequence of human wild-type TRAC1 (SEQ ID NO:2); Figure 1C shows a second, slightly shorter cDNA sequence of human wild type TRAC1 (SEQ ID NO:3); Figure 1D shows a cDNA sequence encoding a truncated version of TRAC1 (SEQ ID NO:4; nucleotides 127-891 of SEQ ID NO:3); Figure 1E shows a genomic sequence of human wild type TRAC1 (SEQ ID NO:5); and Figure 1F shows a cDNA (SEQ ID NO:6) and amino acid sequence (SEQ ID NO:7) for mouse wild type TRAC1.--

Please replace the paragraph beginning at page 6, line 11, with the following:

--Figure 7 shows that TRAC1 (FLJ20456) (SEQ ID NO:1) is similar to two sequences (SEQ ID NOS:8 and 9) with ring domains.--

Please replace the paragraph beginning at page 6, line 21, with the following:

--Figure 13A shows point mutations in conserved cysteine residues of the TRAC1 ring finger domain (SEQ ID NOS:10-17). Figure 13B shows point mutations in the conserved cysteine residues of the TRAC1 ring finger domain disrupt ligase activity.--

Please replace the paragraph beginning at page 12, line 30, with the following:

--The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences

that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., a nucleotide sequence of SEQ ID NO:2), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.--

Please replace the paragraph beginning at page 39, line 22, with the following:

--Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:18). Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 13, at the end of the application.

In the Claims:

Please amend claims 24 and 33 as follows:

24. (Amended) A method for identifying a compound capable of interfering with binding of an TRAC1 polypeptide or fragment thereof, the method comprising the steps of:

(i) combining an TRAC1 polypeptide or fragment thereof with an E2 ubiquitin-conjugating enzyme polypeptide and the compound, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1; and

(ii) determining the binding of the TRAC1 polypeptide or fragment thereof to the E2 ubiquitin-conjugating enzyme polypeptide.

33. (Amended) An isolated complex comprising a TRAC1 polypeptide or fragment thereof bound to an E2 ubiquitin-conjugating enzyme polypeptide, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1.

REMARKS

Claims 1-46 are pending in this application. Claims 24 and 33 have been amended. The amendments to claims 24 and 33 correct the assigned identifiers for SEQ ID NO: designated in these claims. The claim language in claims 24 and 33 refer to amino acid sequences, whereas SEQ ID NO:2 is the corresponding nucleic acid sequence for which the amended SEQ ID NO:1 pertains.

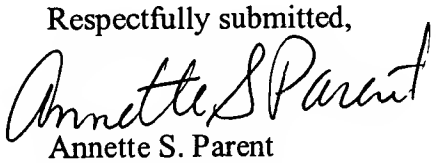
Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-18, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Claims by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."** As a convenience to the Examiner, a complete set of the Claims, as amended herein, is also attached to this Amendment as an Appendix entitled **"PENDING CLAIMS WITH ENTRY OF THE AMENDMENT."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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ASP:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 26 of page 5 has been amended as follows:

Figure 1: Figure 1A shows an amino acid of human wild-type TRAC1 (SEQ ID NO:1); Figure 1B shows a cDNA sequence of human wild-type TRAC1 (SEQ ID NO:2); Figure 1C shows a second, slightly shorter cDNA sequence of human wild type TRAC1 (SEQ ID NO:3); Figure 1D shows a cDNA sequence encoding a truncated version of TRAC1 (SEQ ID NO:4; nucleotides 127-891 of SEQ ID NO:3); Figure 1E shows a genomic sequence of human wild type TRAC1 (SEQ ID NO:5); and Figure 1F shows a cDNA (SEQ ID NO:6) and amino acid sequence (SEQ ID NO:7) for mouse wild type TRAC1.

Paragraph beginning at line 11 of page 6 has been amended as follows:

Figure 7 shows that TRAC1 (FLJ20456) (SEQ ID NO:1) is similar to two sequences (SEQ ID NOS:8 and 9) with ring domains.

Paragraph beginning at line 21 of page 6 has been amended as follows:

Figure 13A shows point mutations in conserved cysteine residues of the TRAC1 ring finger domain (SEQ ID NOS:10-17). Figure 13B shows point mutations in the conserved cysteine residues of the TRAC1 ring finger domain disrupt ligase activity.

Paragraph beginning at line 30 of page 12 has been amended as follows:

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., a nucleotide sequence of SEQ ID NO:2), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length. ~~nu~~

Paragraph beginning at line 22 of page 39 has been amended as follows:

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly Gly ~~gly~~ sequences of between about 5 and 200 amino acids (SEQ ID NO:18). Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

In the Claims:

Claims 24 and 33 have been amended as follows:

24. (Amended) A method for identifying a compound capable of interfering with binding of an TRAC1 polypeptide or fragment thereof, the method comprising the steps of:

(i) combining an TRAC1 polypeptide or fragment thereof with an E2 ubiquitin-conjugating enzyme polypeptide and the compound, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1 ~~SEQ ID NO:2~~; and

(ii) determining the binding of the TRAC1 polypeptide or fragment thereof to the E2 ubiquitin-conjugating enzyme polypeptide.

33. (Amended) An isolated complex comprising a TRAC1 polypeptide or fragment thereof bound to an E2 ubiquitin-conjugating enzyme polypeptide, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1 ~~SEQ ID NO:2~~.

PENDING CLAIMS WITH ENTRY OF THE AMENDMENT

1. (As filed) A method for identifying a compound that modulates T lymphocyte activation, the method comprising the steps of:

(i) contacting the compound with a TRAC1 polypeptide or a fragment thereof, the polypeptide or fragment thereof encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1; and

(ii) determining the functional effect of the compound upon the TRAC1 polypeptide.

2. (As filed) The method of claim 1, wherein the functional effect is measured *in vitro*.

3. (As filed) The method of claim 2, wherein the functional effect is a physical effect.

4. (As filed) The method of claim 2, wherein the functional effect is a chemical effect.

5. (As filed) The method of claim 4, wherein the functional effect is determined by measuring ligase activity.

6. (As filed) The method of claim 1, wherein the polypeptide is expressed in a host cell.

7. (As filed) The method of claim 6, wherein the functional effect is a physical effect.

8. (As filed) The method of claim 6, wherein the functional effect is a chemical or phenotypic effect.

9. (As filed) The method of claim 6, wherein the host cell is primary T lymphocyte.

10. (As filed) The method of claim 6,wherein the host cell is a cultured T cell.

11. (As filed) The method of claim 10, wherein the host cell is a Jurkat cell.

12. (As filed) The method of claim 6, wherein the chemical or phenotypic effect is determined by measuring CD69 expression, intracellular Ca2+ mobilization, Ca2+ influx, ligase activity, or lymphocyte proliferation.

13. (As filed) The method of claim 1, wherein modulation is inhibition of T lymphocyte activation.

14. (As filed) The method of claim 1, wherein the polypeptide is recombinant.

15. (As filed) The method of claim 1, wherein the TRAC1 polypeptide comprises an amino acid sequence of SEQ ID NO:1.

16. (As filed) The method of claim 1, wherein the TRAC1 polypeptide is encoded by a nucleic acid comprising a nucleotide sequence of SEQ ID NO:2.

17. (As filed) The method of claim 1, wherein the compound is an antibody.

18. (As filed) The method of claim 1, wherein the compound is an antisense molecule.

19. (As filed) The method of claim 1, wherein the compound is a small organic molecule.

20. (As filed) The method of claim 1, wherein the compound is a peptide.

21. (As filed) The method of claim 20, wherein the peptide is circular.

22. (As filed) A method for identifying a compound that modulates T lymphocyte activation, the method comprising the steps of:

(i) contacting a T cell comprising a TRAC1 polypeptide or fragment thereof with the compound, the TRAC1 polypeptide or fragment thereof encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1; and

(ii) determining the chemical or phenotypic effect of the compound upon the cell comprising the TRAC1 polypeptide or fragment thereof, thereby identifying a compound that modulates T lymphocyte activation.

23. (As filed) A method for identifying a compound that modulates T lymphocyte activation, the method comprising the steps of:

(i) contacting the compound with a TRAC1 polypeptide or a fragment thereof, the TRAC1 polypeptide or fragment thereof encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1;

(ii) determining the physical effect of the compound upon the TRAC1 polypeptide; and

(iii) determining the chemical or phenotypic effect of the compound upon a cell comprising the TRAC1 polypeptide or fragment thereof, thereby identifying a compound that modulates T lymphocyte activation.

24. (Amended) A method for identifying a compound capable of interfering with binding of an TRAC1 polypeptide or fragment thereof, the method comprising the steps of:

(i) combining an TRAC1 polypeptide or fragment thereof with an E2 ubiquitin-conjugating enzyme polypeptide and the compound, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1; and

(ii) determining the binding of the TRAC1 polypeptide or fragment thereof to the E2 ubiquitin-conjugating enzyme polypeptide.

25. (As filed) The method of claim 24, wherein the TRAC1 polypeptide or fragment thereof has ligase activity.

26. (As filed) The method of claim 24, wherein the E2 ubiquitin-conjugating enzyme polypeptide is selected from the group consisting of Ubc5, Ubc7, and Ubc8.

27. (As filed) The method of claim 24, wherein the TRAC1 polypeptide or fragment thereof and the E2 ubiquitin-conjugating enzyme polypeptide are combined first.

28. (As filed) The method of claim 24, wherein the reaction is performed *in vitro*.

29. (As filed) The method of claim 24, wherein the TRAC1 polypeptide or fragment thereof and the E2 ubiquitin-conjugating enzyme polypeptide are expressed in a cell.

30. (As filed) The method of claim 29, wherein the cell is a yeast cell.

31. (As filed) The method of claim 30, wherein the TRAC1 polypeptide or fragment thereof is fused to a heterologous polypeptide.

32. (As filed) The method of claim 24, wherein the binding of the TRAC1 polypeptide or fragment thereof to the E2 ubiquitin-conjugating enzyme polypeptide is determined by measuring reporter gene expression.

33. (Amended) An isolated complex comprising a TRAC1 polypeptide or fragment thereof bound to an E2 ubiquitin-conjugating enzyme polypeptide, wherein the TRAC1 polypeptide or fragment thereof is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1.

34. (As filed) The complex of claim 33, wherein the E2 ubiquitin-conjugating enzyme polypeptide is selected from the group consisting of Ubc5, Ubc7, and Ubc8.

35. (As filed) A method of modulating T lymphocyte activation in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified using the method of claim 1.

36. (As filed) The method of claim 35, wherein the subject is a human.

37. (As filed) The method of claim 35, wherein the compound is an antibody.

38. (As filed) The method of claim 35, wherein the compound is an antisense molecule.

39. (As filed) The method of claim 35, wherein the compound is a small organic molecule.

40. (As filed) The method of claim 35, wherein the compound is a peptide.

41. (As filed) The method of claim 40, wherein the peptide is circular.

42. (As filed) The method of claim 35, wherein the compound inhibits T lymphocyte activation.

43. (As filed) A method of modulating T lymphocyte activation in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a TRAC1 polypeptide, the polypeptide encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1.

44. (As filed) The method of claim 43, wherein the TRAC1 polypeptide comprises an amino acid sequence of SEQ ID NO:1.

45. (As filed) A method of modulating T lymphocyte activation in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a nucleic acid encoding a TRAC1 polypeptide, wherein the nucleic acid hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:1.

46. (As filed) The method of claim 45, wherein the TRAC1 nucleic acid comprises a nucleotide sequence of SEQ ID NO:2.